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ORIGINAL RESEARCH

Genetic diversity and antibiotic resistance of *Shigella* spp. isolates from food products

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Abstract

The emergence of multidrug-resistant *Shigella* is a significant threat to global public health. Limited studies have investigated the incidence, antimicrobial susceptibility, and genetic diversity of *Shigella* isolated from food products. Conventional culture-based, serologic, molecular, disk diffusion, PCR, and RAPD-PCR methods were used to determine the prevalence rate, phenotypic and genotypic antibiotic resistance profile, and genetic diversity of the *Shigella* isolates from food samples including vegetable salad, ground meat, and raw cow's milk (405 samples). The prevalence rate of *Shigella* in food samples was 4.44%. The incidence of *S. sonnei* (3.7%) was higher than that of *S. flexneri* (0.74%). *S. dysenteriae* and *S. boydii* were not detected in food samples examined. Also, no *Shigella* were recovered from raw cow's milk. This study showed that the *Shigella* isolates were resistant to sulfamethoxazole/trimethoprim (83.3%), amoxicillin (66.6%), streptomycin (66.6%), tetracycline (61.1%), ampicillin (50%), amoxicillin–clavulanic acid (50%), azithromycin (50%), and chloramphenicol (50%) and completely sensitive to cefoxitin, cefepime, amikacin, and gentamicin. All *Shigella* isolates were multidrug-resistant. We detected bla_{SHV} resistance gene in all isolates; however, no isolate harbored bla_{TEM} gene. RAPD-PCR categorized the *Shigella* isolates into five main clusters. The highest antibiotic resistance was observed in the isolates of cluster R4. The finding of this study also indicated an association between antimicrobial resistance profiles and genotyping properties of the isolates. Novel food monitoring systems, including surveillance of multidrug-resistant foodborne pathogens, especially in developing countries, are required to control the foodborne diseases.

KEYWORDS

antimicrobial resistance, food samples, genetic diversity, *Shigella* species